

# SEQUENCE LISTING

<110> Kapeller-Libermann, Rosana

<120> 58860, A HUMAN CHOLESTERYL ESTER  
HYDROLASE AND USES THEREFOR

<130> MPI2001-026P1RCP1(M)

<150> 60/264,167

<160> 6

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<210> 1

<211> 1325

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (16)...(1212)

<400> 1

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      Met Met Trp Leu Leu Leu Thr Thr Thr Cys Leu Ile
              1              5              10

tgt gga act tta aat gct ggt gga ttc ctt gat ttg gaa aat gaa gtg   99
Cys Gly Thr Leu Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val
      15              20              25

aat cct gag gtg tgg atg aat act agt gaa atc atc atc tac aat ggc   147
Asn Pro Glu Val Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly
      30              35              40

tac ccc agt gaa gag tat gaa gtc acc act gaa gat ggg tat ata ctc   195
Tyr Pro Ser Glu Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu
      45              50              55              60

ctt gtc aac aga att cct tat ggg cga aca cat gct agg agc aca ggt   243
Leu Val Asn Arg Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly
      65              70              75

ccc cgg cca gtt gtg tat atg cag cat gcc ctg ttt gca gac aat gcc   291
Pro Arg Pro Val Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala
      80              85              90

tac tgg ctt gag aat tat gct aat gga agc ctt gga ttc ctt cta gca   339
Tyr Trp Leu Glu Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala
      95              100              105

gat gca ggt tat gat gta tgg atg gga aac agt cgg gga aac act tgg   387
Asp Ala Gly Tyr Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp
      110              115              120

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tca Ser 125	aga Arg	aga Arg	cac His	aaa Lys	aca Thr 130	ctc Leu	tca Ser	gag Glu	aca Thr	gat Asp 135	gag Glu	aaa Lys	ttc Phe	tgg Trp	gcc Ala 140	435
ttt Phe	agt Ser	ttt Phe	gat Asp 145	gaa Glu	atg Met	gcc Ala	aaa Lys	tat Tyr	gat Asp 150	ctc Leu	cca Pro	gga Gly	gta Val	ata Ile 155	gac Asp	483
ttc Phe	att Ile	gta Val 160	aat Asn	aaa Lys	act Thr	ggg Gly	cag Gln	gag Glu 165	aaa Lys	ttg Leu	tat Tyr	ttc Phe	att Ile 170	gga Gly	cat His	531
tca Ser	ctt Leu 175	ggc Gly	act Thr	aca Thr	ata Ile	ggg Gly	ttt Phe 180	gta Val	gcc Ala	ttt Phe	tcc Ser	acc Thr 185	atg Met	cct Pro	gaa Glu	579
ctg Leu 190	gca Ala	caa Gln	aga Arg	atc Ile	aaa Lys 195	atg Met	aat Asn	ttt Phe	gcc Ala	ttg Leu 200	ggg Gly	cct Pro	acg Thr	atc Ile	tca Ser	627
ttc Phe 205	aaa Lys	tat Tyr	ccc Pro	acg Thr 210	ggc Gly	att Ile	ttt Phe	acc Thr	agg Arg 215	ttt Phe	ttt Phe	cta Leu	ctt Leu	cca Pro	aat Asn 220	675
tcc Ser	ata Ile	atc Ile	aag Lys 225	gct Ala	gtt Val	ttt Phe	ggg Gly	acc Thr 230	aaa Lys	ggg Gly	ttc Phe	ttt Phe	tta Leu	gaa Glu 235	gat Asp	723
aag Lys	aaa Lys	acg Thr 240	aag Lys	ata Ile	gct Ala	tct Ser	acc Thr 245	aaa Lys	atc Ile	tgc Cys	aac Asn	aat Asn 250	aag Lys	ata Ile	ctc Leu	771
tgg Trp	ttg Leu 255	ata Ile	tgt Cys	agc Ser	gaa Glu	ttt Phe	atg Met 260	tcc Ser	tta Leu	tgg Trp	gct Ala 265	gga Gly	tcc Ser	aac Asn	aag Lys	819
aaa Lys 270	aat Asn	atg Met	aat Asn 275	cag Gln	agt Ser	cga Arg	atg Met 280	gat Asp	gtg Val	tat Tyr 285	atg Met 290	tca Ser	cat His	gct Ala	ccc Pro	867
act Thr 285	ggg Gly	tca Ser	tca Ser	gta Val 290	cac His	aac Asn	att Ile	ctg Leu	cat His 295	ata Ile	aaa Lys	cag Gln	ctt Leu	tac Tyr	cac His 300	915
tct Ser	gat Asp	gaa Glu	ttc Phe 305	aga Arg	gct Ala	tat Tyr	gac Asp	tgg Trp 310	gga Gly	aat Asn	gac Asp	gct Ala	gat Asp	aat Asn 315	atg Met	963
aaa Lys	cat His	tac Tyr 320	aat Asn	cag Gln	agt Ser	cat His	ccc Pro 325	cct Pro	ata Ile	tat Tyr	gac Asp	ctg Leu	act Thr 330	gcc Ala	atg Met	1011
aaa Lys	gtg Val 335	cct Pro	act Thr	gct Ala	att Ile	tgg Trp	gct Ala 340	ggg Gly	gga Gly	cat His	gat Asp	gtc Val 345	ctc Leu	gta Val	aca Thr	1059

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ccc cag gat gtg gcc agg ata ctc cct caa atc aag agt ctt cat tac 1107
Pro Gln Asp Val Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr
    350                355                360

ttt aag cta ttg cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc 1155
Phe Lys Leu Leu Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu
365                370                375                380

gat gcc cct caa cgg atg tac agt gaa atc ata gct tta atg aag gca 1203
Asp Ala Pro Gln Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala
    385                390                395

tat tcc taa atggaaaaaa aaaaaaaaaa aaaaaaaaaa aaagcggccg 1252
Tyr Ser *
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ctgaattcta gacctgcccg ggccggccgct cgagccctat agtgagtaag ggcgaattcg 1312
cgcccgctaa att 1325
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<210> 2
<211> 398
<212> PRT
<213> Homo sapiens
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<400> 2
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Met Met Trp Leu Leu Leu Thr Thr Thr Cys Leu Ile Cys Gly Thr Leu
 1          5          10          15
Asn Ala Gly Gly Phe Leu Asp Leu Glu Asn Glu Val Asn Pro Glu Val
 20          25          30
Trp Met Asn Thr Ser Glu Ile Ile Ile Tyr Asn Gly Tyr Pro Ser Glu
 35          40          45
Glu Tyr Glu Val Thr Thr Glu Asp Gly Tyr Ile Leu Leu Val Asn Arg
 50          55          60
Ile Pro Tyr Gly Arg Thr His Ala Arg Ser Thr Gly Pro Arg Pro Val
 65          70          75          80
Val Tyr Met Gln His Ala Leu Phe Ala Asp Asn Ala Tyr Trp Leu Glu
 85          90          95
Asn Tyr Ala Asn Gly Ser Leu Gly Phe Leu Leu Ala Asp Ala Gly Tyr
100          105          110
Asp Val Trp Met Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Arg His
115          120          125
Lys Thr Leu Ser Glu Thr Asp Glu Lys Phe Trp Ala Phe Ser Phe Asp
130          135          140
Glu Met Ala Lys Tyr Asp Leu Pro Gly Val Ile Asp Phe Ile Val Asn
145          150          155          160
Lys Thr Gly Gln Glu Lys Leu Tyr Phe Ile Gly His Ser Leu Gly Thr
165          170          175
Thr Ile Gly Phe Val Ala Phe Ser Thr Met Pro Glu Leu Ala Gln Arg
180          185          190
Ile Lys Met Asn Phe Ala Leu Gly Pro Thr Ile Ser Phe Lys Tyr Pro
195          200          205
Thr Gly Ile Phe Thr Arg Phe Phe Leu Leu Pro Asn Ser Ile Ile Lys
210          215          220
Ala Val Phe Gly Thr Lys Gly Phe Phe Leu Glu Asp Lys Lys Thr Lys
225          230          235          240
Ile Ala Ser Thr Lys Ile Cys Asn Asn Lys Ile Leu Trp Leu Ile Cys
245          250          255
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Ala Ile Trp Ala Gly Gly His Asp Val Leu Val Thr Pro Gln Asp Val  
 340 345 350

gcc agg ata ctc cct caa atc aag agt ctt cat tac ttt aag cta ttg 1104  
 Ala Arg Ile Leu Pro Gln Ile Lys Ser Leu His Tyr Phe Lys Leu Leu  
 355 360 365

cca gat tgg aac cac ttt gat ttt gtc tgg ggc ctc gat gcc cct caa 1152  
 Pro Asp Trp Asn His Phe Asp Phe Val Trp Gly Leu Asp Ala Pro Gln  
 370 375 380

cgg atg tac agt gaa atc ata gct tta atg aag gca tat tcc 1194  
 Arg Met Tyr Ser Glu Ile Ile Ala Leu Met Lys Ala Tyr Ser  
 385 390 395

<210> 4  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 4  
 Phe Arg Val Ile Ala Leu Asp Leu Arg Gly Phe Gly Glu Ser Ser Arg  
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 Pro Ser Asp Leu Ala Asp Tyr Arg Phe Asp Asp Leu Ala Glu Asp Leu  
 20 25 30  
 Glu Ala Leu Leu Asp Ala Leu Gly Leu Asp Lys Pro Val Ile Leu Val  
 35 40 45  
 Gly His Ser Met Gly Gly Ala Leu Ala Ala Tyr Ala Ala Lys Tyr  
 50 55 60  
 Pro Glu Glu Arg Val Lys Ala Leu Val Leu Val Ser Thr Pro Ala Pro  
 65 70 75 80  
 Ala Gly Leu Ser Ser Arg Leu Phe Pro Arg Leu Gly Asn Leu Glu Gly  
 85 90 95  
 Leu Leu Leu Ala Asn Phe Phe Asn Arg Leu Ser Arg Ser Val Glu Ala  
 100 105 110  
 Leu Leu Gly Arg Ala Leu Lys Gln Phe Phe Leu Leu Gly Arg Pro Phe  
 115 120 125  
 Val Ser Asp Phe Leu Lys Gln Ala Glu Asp Trp Leu Ser Ser Leu Ala  
 130 135 140  
 Arg Pro Gly Glu Thr Asp Gly Gly Asp Gly Leu Leu Gly Tyr Ala Val  
 145 150 155 160  
 Ala Leu Gly Lys Leu Leu Gln Trp Asp Arg Ser Ala Leu Lys Asp Ile  
 165 170 175  
 Lys Val Pro Thr Leu Val Ile Trp Gly Asp Asp Asp Pro Leu Val Pro  
 180 185 190  
 Leu Lys Ala Ser Glu Lys Leu Ser Ala Leu Phe Pro Asn Ala Glu Val  
 195 200 205  
 Val Val Ile Asp Asp Ala Gly His Leu Ala Leu Leu Glu Lys Pro Glu  
 210 215 220  
 Glu Val Ala Glu Leu Ile Lys Phe Leu  
 225 230

<210> 5  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 5

Trp Ile Ala Asn Gly Pro Asn Lys Ser Leu Ala Phe Ile Leu Ala Asp  
1 5 10 15  
Ala Gly Tyr Asp Val Trp Leu Gly Asn Ser Arg Gly Asn Thr Tyr Ser  
20 25 30  
Arg Lys His Val Lys Leu Asn Pro Ser His Ser Glu Phe Trp Asp Phe  
35 40 45  
Ser Trp His Glu Met Gly Met Tyr Asp Leu Pro Ala Met Ile Asp Tyr  
50 55 60  
Val Leu Glu Thr Thr Gly Gln Glu Lys Leu His Tyr Val Gly His Ser  
65 70 75 80  
Gln Gly Thr Thr Val Phe Phe Val Met Leu Ser Glu Arg Pro Glu Tyr  
85 90 95  
Asn Glu Lys Ile Lys Ser Phe His Ala Leu Ala Pro Val Ala Tyr Met  
100 105 110  
Lys His Val Arg Ser Pro Leu Val Lys Leu Leu Ala Pro Gln Ser

<210> 6

<211> 10

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (1)...(1)

<223> The amino acid at position 1 can be I or V

<223> The amino acid at position 2 can be any amino acid

<221> VARIANT

<222> (3)...(3)

<223> The amino acid at position 3 can be I or V or M or  
S or T

<221> VARIANT

<222> (4)...(4)

<223> the amino acid at position 4  
can be I or V or M or S or T

<221> VARIANT

<222> (6)...(6)

<223> the amino acid at position 6 can be Y or W or V

<223> The amino acid at position 8  
can be any amino acid

<221> VARIANT

<222> (10)...(10)

<223> The amino acid at position 10 can be S or T or A  
or C

<400> 6

Leu Xaa Leu Leu Gly His Ser Xaa Gly Gly  
1 5 10